

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Original) A process for the enhanced production of pantothenate, comprising culturing a microorganism having a deregulated methylenetetrahydrofolate (MTF) biosynthetic pathway, under conditions such that pantothenate production is enhanced.
2. (Original) A process for the enhanced production of pantothenate, comprising culturing a microorganism having
 - (i) a deregulated pantothenate biosynthetic pathway, and
 - (ii) a deregulated methylenetetrahydrofolate (MTF) biosynthetic pathway,under conditions such that pantothenate production is enhanced.
3. (Original) The process of claim 2, wherein said microorganism has at least two pantothenate biosynthetic enzymes deregulated.
4. (Original) The process of claim 2, wherein said microorganism has at least three pantothenate biosynthetic enzymes deregulated.
5. (Original) The process of claim 2, wherein said microorganism has at least four pantothenate biosynthetic enzymes deregulated.
6. (Original) The process of claim 5, wherein said microorganism has a deregulated ketopantoate hydroxymethyltransferase, a deregulated ketopantoate reductase, a deregulated pantothenate synthetase and a deregulated aspartate- α -decarboxylase.
7. (Previously Presented) The process of claim 1 or 2, wherein said microorganism further has a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.

8. (Original) The process of claim 7, wherein said microorganism has at least two isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
9. (Original) The process of claim 7, wherein said microorganism has at least three isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
10. (Original) The process of claim 9, wherein said microorganism has a deregulated acetohydroxyacid acid synthetase, a deregulated acetohydroxyacid isomeroreductase, and a deregulated dihydroxyacid dehydratase.
11. (Currently Amended) The process of claims 1 or 2 ~~any one of claims 1 to 10~~, wherein the microorganism has at least one MTF biosynthetic enzyme deregulated.
12. (Original) The process of claim 11, wherein the microorganism has a deregulated *glyA* gene.
13. (Original) The process of claim 11, wherein the microorganism has a deregulated *serA* gene.
14. (Original) The process of claim 11, wherein the microorganism has a deregulated *glyA* gene and a deregulated *serA* gene.
15. (Original) The process of claim 12 or 14, wherein the microorganism has a mutated, deleted or disrupted *purR* gene.
- 16.-22. (Canceled)
23. (Currently Amended) The process of claim 1 or 2 ~~any one of the preceding claims~~, wherein pantothenate production is further enhanced by regulating pantothenate kinase activity.
- 24.-27. (Canceled)
28. (Currently Amended) The process of claim 1 or 2 ~~any one of the above claims~~, wherein said microorganism is cultured under conditions of excess serine.

29.-30. (Canceled)

31. (Currently Amended) The process of claim 1 or 2, ~~any one of the above claims~~ wherein the microorganism is a Gram positive microorganism.

32. (Currently Amended) The process of claim 1 or 2, ~~any one of the above claims~~ wherein the microorganism belongs to the genus *Bacillus*.

33. (Currently Amended) The process of claim 1 or 2 ~~any one of the above claims~~, wherein the microorganism is *Bacillus subtilis*.

34.-49. (Canceled)

50. (New) The process of claim 1 or 2, wherein the microorganism overexpresses relative to a wild-type cell at least one methylenetetrahydrofolate (MTF) biosynthetic enzyme encoded by a gene selected from the group consisting of *glyA*, *serA*, *serC*, *serB*, *gcvT*, *gcvPA*, *gcvPB*, and *gcvH* overexpressed.

51. (New) The process of claim 15, wherein the microorganism overexpresses the *glyA* gene as a result of a mutation in the *purR* repressor gene.

52. (New) The process of claim 15, wherein the microorganism further has a deregulated methylenetetrahydrofolate (MTF) biosynthetic enzyme encoded by a gene selected from the group consisting of *glyA*, *serA*, *serC*, *serB*, *gcvT*, *gcvPA*, *gcvPB*, and *gcvH*.

53. (New) The process of claim 15, wherein the microorganism further has a deregulated pantothenate biosynthetic pathway.

54. (New) The process of claim 53, wherein said microorganism has at least two pantothenate biosynthetic enzymes deregulated.

55. (New) The process of claim 53, wherein said microorganism has at least three pantothenate biosynthetic enzymes deregulated.

56. (New) The process of claim 53, wherein said microorganism has at least four pantothenate biosynthetic enzymes deregulated.
57. (New) The process of claim 56, wherein said microorganism has a deregulated ketopantoate hydroxymethyltransferase, a deregulated ketopantoate reductase, a deregulated pantothenate synthetase and a deregulated aspartate- α -decarboxylase.
58. (New) The process of claim 15, wherein said microorganism further has a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.
59. (New) The process of claim 58, wherein said microorganism has at least two isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
60. (New) The process of claim 58, wherein said microorganism has at least three isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
61. (New) The process of claim 60, wherein said microorganism has a deregulated acetohydroxyacid acid synthetase, a deregulated acetohydroxyacid isomeroreductase, and a deregulated dihydroxyacid dehydratase.
62. (New) The process of claim 15, wherein said microorganism is cultured under conditions of excess serine.
63. (New) The process of claim 15, wherein the microorganism is a Gram positive microorganism.
64. (New) The process of claim 15, wherein the microorganism belongs to the genus *Bacillus*.
65. (New) The process of claim 15, wherein the microorganism is *Bacillus subtilis*.